Fig. 1

1) ygbB
atgcgaattggacacggttttgacgtacatgcctttggcggtgaaggcccaattatcattggtggcgtacgcattccttacgaaaa
aggattgctggcgcattctgatggcgacgtggcgctccatgcgttgaccgatgcattgcttggcgcggcggcgctgggggggat
cggcaagctgttcccggataccgatccggcatttaaaggtgccgatagccgcgagctgctacgcgaagcctggcgtcgtattc
aggcgaagggttatacccttggcaacgtcgatgtcactatcatcgctcaggcaccgaagatgttgccgcacattccacaaatg
cgcgtgtttattgccgaagatctcggctgccatatggatgatgttaacgtgaaagccactactacggaaaaactgggatttaccg
gacgtggggaagggattgcctgtgaagcggtggcgctactcattaaggcaacaaaatga (SEQ ID NO: 16)

2) yfhC
atgcgccgcgcttttataaccggagttttctttttgtctgaagtcgaatttagccacgaatactggatgcgtcacgcgctgacgctg
gcgaaacgtgcctgggatgagcgggaagtgccggtcggcgcggtattagtgcataacaatcgggtaatcggcgaaggctg
gaaccgcccgattggtcgccatgatcccaccgcacatgcagaaatcatggccctgcggcagggtggtctggtgatgcaaaat
tatcgtctgatcgacgccacgttgtatgtcacgcttgaaccatgtgtaatgtgtgccggagcgatgatccacagtcgcattggtcg
cgtggtctttggtgcgcgtgacgcgaaaactggcgctgcgggatctttaatggatgtgctgcatcatccgggtatgaatcaccga
gtggaaattacggaaggaatactggcggatgagtgcgcggcgttgctcagtgacttctttcgcatgcgccgccaggaaattaa
agcgcagaaaaaagcgcaatcctcgacggattaa (SEQ ID NO: 17)

3) yacE
atgaggtatatagttgccttaacgggggaggcattggcagtggcaagagtaccgttgccaatgcgtttgctgatctcggaattaacg
tcattgatgccgatattattgcgcgtcaggtggttgaaccaggtgcacctgcgctacatgccattgctgatcactttggcgctaaca
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tggcagatgacgtcattgataataacggcgcaccggatgctatcgcatcggatgttgcccgcctgcacgcacactatttgcagc
ttgcgtcgcagtttgtctcacaggaaaaaccgtaa (SEQ ID NO: 18)

4) ychB
atgcggacacagtggccctctccggcaaaacttaatctgtttttatacattaccggtcagcgtgcggatggttaccacacgctgc
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aagcccgccaggtgctagagcaagccccggaatggctcaatggctttgtggcgaaaggcgctaatctttccccattgcacag
agccatgctttaa (SEQ ID NO: 19)

5) yejD
atgcgacttgataaatttatcgcacagcaactcggccgttagccgtgctattgccgggcgtgaaatccgcggcaatcgtgtcacc
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gacgatacggcagagcaatttgctaaaggcgtgcagctgcataacgaaaaagatctcactaagcctgcggtgctggaagtg
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cgtggttgagctgcatcgtgaacgtattggcggtattacgctggatgctgatttagcccccggtgaatatcgtccgttaactgaag
aagaaattgccagcgtcgtctaa (SEQ ID NO: 20)

6) yrfI

atgattatgccgcaacatgaccaattacatcgctatctgtttgaaaactttgccgtgcgcggcgaactggtaaccgtttcggaaa
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gcaatggttacgtggtgatcaccattaccccgagcgaaggcgaacgctatcagggcgtagttggtctggaaggtgataccctg
gcggcctgcctggaagattactttatgcgttctgaacagctgccgacgcgcctgtttattcgcaccggcgacgtagacggcaaa
ccggctgcaggcggtatgttgttgcaggtaatgcctgcgcaaaatgcccagcaggacgactttgaccacctggcgacgctaa
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cggtttacgatccgcaggatgtggagttcaaatgcacctgctcgcgtgaacgttgcgccgatgcgctgaaaacgctgcctgatg
aagaagttgatagcatcctggcggaagatggcgaaattgacatgcattgtgattactgcggtaaccactatctgttcaatgcgat
ggatattgctgaaatccgcaacaacgcgtctccggcagatccgcaagttcattaa (SEQ ID NO: 21)

7) yggJ

gtggggagacgacgcggattttttaactatgcgtatcccccgcatttatcatcctgaaccactgaccagccattctcacatcgcgct
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ggctaa (SEQ ID NO: 22)

8) yjeE

atgatgaatcgagtaattccgctccctgatgagcaggcaacattagacctgggcgagcgggtagcgaaagcctgcgatggc
gcaaccgtaatctatctgtatggcgatttaggcgcaggtaaaaaccacctttagccggggcttttacaggctctgggtcatcagg
gtaatgtcaaaagcccccacttatacgctggtcgaaccctatacgctcgacaacttaatggtctatcactttgatttgtaccgccttg
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(SEQ ID NO: 23)

9) yiaO

atgaaattacgctctgtaacctacgcattattcattgctggcctggctgcattcagcacatcttctctggcggcacaatctttacgttt
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24)

10) yrdC

gtgaataataacctgcaaagagacgctatcgcagctgcgatagatgttctcaatgaagaacgtgtcatcgcctatccaacgga
agccgttttcggtgttgggtgcgatcctgatagcgaaacagcagtgatgcgactgttggagttaaaaacagcgtccggttgataa
ggggctgattttaatcgcagcaaattacgagcagcttaaaccctatattgatgacaccatgttgactgacgtgcagcgtgaaac
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Fig. 1 continued

cttgctgtacgagtcaccgaccatccgttggtggttgctttgtgccaggcttatggtaaaccgctggtttctaccagtgccaacttga
gtggattgccaccttgtcgaacagtagacgaagttcgcgcacaatttggcgcggcgttcccggttgtgcctggtgaaacggg
gggcgtttaaatccttcagaaatccgcgatgccctgacgggtgaactgtttcgacagggggtaa (SEQ ID NO: 25)

11) yhbC

gtgggcttgtccacattagagcaaaaattaacagagatgattactgcgccagttgaggccctgggttttgaactggttggcatcg
aatttattcgcggtcgcacatccacactgcgcatctatattgatagtgaagatggcatcaatgttgatgattgtgctgatgtgagcc
accaggtaagtgctgtgctggatgttgaagatcccatcaccgttgcttataacctggaagtctcctcaccgggtctcgatcgccc
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atggcagggcgttatcaaagcggtagacggtgaaatgatcacagttaccgtcgaaggtaaagatgaagtgttcgcgctgagt
aatatccagaaggcgaacctggttccccactttaa (SEQ ID NO: 26)

12) ygbP

atggcaaccactcatttggatgtttgcgccgtggttccggcggccggatttggccgtcgaatgcaaacggaatgtcctaagcaa
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tattgcggattccatcctcagttggtcgaaggccgtgcggataacattaaagtcacgcgcccggaagatttggcactggccga
gttttacctcacccgaaccatccatcaggagaatacataa (SEQ ID NO: 27)

13) ybeY

atgagtcaggtgatcctcgatttacaactggcatgtgaagataattccgggttaccggaagagagccagtttcagacatggctg
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14) gcpE

atgcataaccaggctccaattcaacgtagaaaatcaacacgtatttacgttgggaatgtgccgattggcgatggtgctcccatc
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caaagaccgtctggacaacaacgatatgatcgaccagctggaagcacgcattcgtgcgaaagccagtcagctggacgaa
gcgcgtcgaattgacgttcagcaggttgaaaaataa
(SEQ ID NO: 29)

15) kdtB

atgcaaaaacgggcgatttatccgggtactttcgatcccattaccaatggtcatatcgatatcgtgacgcgcgccacgcagatgt
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atgtcacccatttcctgccggagaatgtccatcaggcgctgatggcgaagttagcgtag (SEQ ID NO: 30)

16) pfs

atgaaaatcggcatcattggtgcaatggaagaagaagttacgctgctgcgtgacaaaatcgaaaaccgtcaaactatcagtc
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gacgtggccgatcaacagtctcatcttagcttcgatgagttcctggctgttgccgctaaacagtccagcctgatggttgagtcact
ggtgcagaaacttgcacatggctaa (SEQ ID NO: 31)

17) ycaJ

gtgagcaatctgtctcgctcgattttttcggataatactttcaacctctggccgcgcgtatgcggccagaaaatttagcacagtatatc
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ccgttaa (SEQ ID NO: 32)

18) b1808

gtgacggacgattttgcaccagacggtcagctggcgaaagcgataccaggctttaagccgcgagaaccacagcgacagat
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aagggcaactgttgcagcaatttgtcagcgccggtaatgcgcttcttgtggcaaccagcagtttctgggaaggggtggacgtgc
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Fig. 1 continued

tgtcgtttgcgcggtggcgacccgttcgatgaagtgcaactaccagatgccgtcattactctcaaacagggggtagggcgact
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NO: 33)

19) yeaA

atggctaataaaccttcggcagaagaactgaaaaaaaaatttgtccgagatgcagttttacgtgacgcagaatcatgggacag
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acatggaatgcagcgcatagaaattcgttgcggtaactgtgatgcccatctggggcatgtcttccccgacgggccgcagccaa
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ID NO: 34)

20) yagF

atgaccattgagaaaattttcacccocgcaggacgacgcgtttattgcggtgatcacccacgcggcgggggccgcagggcgctc
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acgccaacaagctcaccggcaaagaggtgctgattatcggcactcagggcggcatccgcgccggagacggacgcccaat
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ccgcaacgacgcggcgatcgtgtttcgccgcctgatccgctccctgccgacgcggcgggcggtgatcggcgtagcgacctg
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gctgccgccgaccgtcggggaagacgcgggcaaggtgcagaccatcggcgcgcgtttcgccaaccacgaactctccctgc
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gcccgccagtcggcgcgcgcggtcagcgagctggatagccgcggcatcaccacgcgggatatcctctccgataaagccat
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cgtcggtggtgggcgaagatggcgtataccaccacaccggccgggtgcgggtgtttgtctcggaagcgcaggcgatcaagg
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gctgtgggcggcactgcagtcggtgagcggcggcacctggaaaggctgtatttatgacaccgataaaattatcgaggtaatta
acgccggtaaaaaagcgctcggaatttaa (SEQ ID NO: 35)

21) b1983

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22) yidD

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cgcattgtcgtttcactccaacctgttcaagctacggaattgaggcattgcgcaggtttggagtgataaaaggcagttggttgacg

Fig. 1 continued

gtgaaacgcgtattaaaatgccaccctttacaccctggtggtgacgatcccgtcccgcccggaccatttgataccagagaaca
ctaa (SEQ ID NO: 37)

23) yceG

atgaaaaaagtgttattgataatcttgttattgctggtggtactgggtatcgccgctggtgtgggcgtctggaaggttcgccatcttg
ccgacagcaaattgcttatcaaagaagagacgatatttaccctgaagccagggaccggacgtctggcgctcggtgaacagc
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(SEQ ID NO:38)

24) yjbC

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cgcgatttaaccgacgatgagttaatcgacctctttaagctcattgaaaattcctcttccgaggtaaaacctaaagcgaaggcc
aaaccgaaaacagcgggcatcaaacgtccagtcgttaagatggaaaaaacggcggaaaaaggcggtcgcccggcgtcc
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Fig. 1 continued
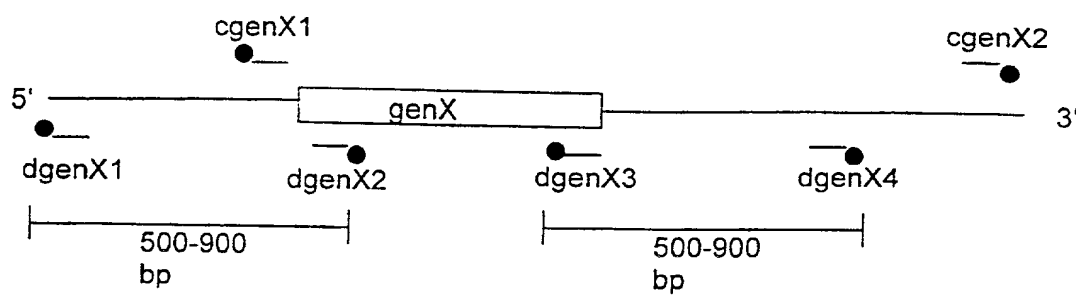
Fig. 2

E. coli		B. subtilis				H. influenzae			H. pylori		
gene name	GenBank#[1]	gene name	SWIPL[2] or Subtilist#[3]	score	E-value	GenBank#[1]	score	E-value	GenBank#[1]	score	E-value
YgbB	g1789103	YacN	[2]Q06/56	169	2,00E-43	1573672	205	1,00E-54	2314164	105	1,00E-24
Ythc	g1788911	YaaJ	[2]P21335	135	2,00E-33	1573925	175	1,00E-45	2313814	24	3
YacE	g1786292	YtbG	[3]BG13824	135	2,00E-33	1573909	191	2,00E-50	2313965	87	4,00E-19
YchB	g1787459	YabH	[2]P37550	102	3,00E-23	1574450	317	3,00E-88	2314615	41	5,00E-05
YcjD	g1788510	YtzF	[3]BG13940	126	6,00E-32	1574175	276	2,00E-74	2314637	61	5,00E-11
Yfll	g1789804	YacC	[2]P37565	71	1,00E-13	1573822	206	5,00E-79	2314107	24	5,4
YggJ	g1789315	YqeU	[2]P54461	96	2,00E-21	1573272	312	1,00E-86	2313478	49	1,00E-07
Yjcl	g1790610	YdiB	[3]BG12199	89	3,00E-19	1573014	171	1,00E-44	2313940	46	9,00E-07
YfaO	g1790004	YdbE	[3]BG12072	148	7,00E-37	1574060	374	1,00E-105	2314105	26	1,5
YfcC	g236/210	YwiC	[2]P39153	93	3,00E-19	1573655	206	3,00E-55	2313122	29	0,13
YlbC	g1789561	YlxS	[2]P32/26	90	1,00E-19	1574740	157	2,00E-40	2314193	65	1,00E-12
Yqpl	g1789104	YacM	[2]Q06/55	129	3,00E-31	1573673	233	4,00E-63	2314164	47	5,00E-07
YbeY	g1788880	YqjG	[2]P46347	70	8,00E-14	1572948	190	2,00E-50	2314318	54	3,00E-09
Cepl	g1788863	YqjY	[2]P54482	318	4,00E-88	1573337	604	1,00E-174	2313753	294	3,00E-81
KdtB	g1790065	Ylbl	[3]BG13361	145	2,00E-36	1573650	176	5,00E-46	2314651	170	3,00E-44
pfs	g1786354	YrrU	[3]BG13800	244	6,00E-66	1574146	254	2,00E-69	2313168	123	4,00E-30
YcaJ	g1787119	YrvN	[3]BG13808	275	5,00E-75	1574435	668	0	2314168	201	3,00E-53
b1808	g1788110	DinG	[2]P54394	245	6,00E-66	1573357	768	0	2313340	33	0,025
yeaA	g1788077	YppQ	[2]P54155	136	2,00E-32	1574293	116	3,00E-28	2313314	125	6,00E-31
ygpl	g1786464	llvD	[2]P51785	180	4,00E-46	1573744	168	1,00E-43	2314249	103	2,00E-23
b1803	g1788294	Yeel	[3]BG12824	279	1,00E-76	1573285	161	2,00E-41	2313249	108	1,00E-25
YfiD	g140861	YljA	[3]BG13865	90	6,00E-19	1176311	96	1,00E-20	2314625	40	8,00E-04

[1] http://www.ncbi.nlm.nih.gov/Entrez/protein.html
[2] http://www.expasy.ch/sprot/
[3] http://www.pasteur.fr/Bio/SubtiList.html
[4] (http://www.ncbi.nlm.nih.gov/BLAST/unfinishedgenome.html)

Fig. 3

E. coli gene name	GenBank#[1]	M. tuberculosis GenBank#[1]	score	E-value	Ch. trachomatis GenBank#[1]	score	E-value	B. burgdorferi GenBank#[1]	score	E-value
YghB	g1789103	1877312	78	1,00E-16	3328865	62	1,00E-12	2688040	23	4,60E+00
YihC	g1788911	2960176	119	1,00E-28	3329316	120	2,00E-29	2687969	23	5,20E+00
YacL	g1786292	2113915	119	1,00E-28	3328928	62	1,00E-11	2688463	41	2,00E-05
YchB	g1787459	2052148	84	1,00E-17	3329270	82	2,00E-17	2688545	23	6,80E+00
Yej0	g1788510	2326754	109	2,00E-25	3329180	105	8,00E-25	2688006	90	5,00E-20
Ytf	g1789804	1550650	25	6,40E+00	3329168	23	7,80E+00	2688577	23	5,40E+00
Ypp	g1789315	2078027	70	2,00E-13	3328922	23	8,60E+00	2688252	44	4,00E-06
YjeE	g1790610	1449365	60	1,00E-10	3328975	61	2,00E-11	2688077	60	1,00E-13
YfaO	g1790004	2113942	27	1,80E+00	3328868	26	1,30E+00	2688570	25	2,70E+00
YidC	g2367210	1322425	68	8,00E-13	3328537	68	2,00E-13	2688669	73	3,00E-15
YhbC	g1789561	2078017	56	2,00E-09	3328787	26	4,00E-01	2688749	38	1,00E-04
YqhP	g1789104	1877313	99	3,00E-22	3328896	95	2,00E-21	2688781	26	6,30E-01
YbeY	g1786880	2078032	62	3,00E-11	3328852	26	4,20E-01	2687941	55	6,00E-10
GcpF	g1788863	2612813	277	9,00E-76	3328450	155	2,00E-39	2688019	31	5,30E-02
KdtB	g1790065	1694866	140	8,00E-35	3329163	25	9,40E-01	2688628	97	2,00E-22
pfs	g1786354	1405762	100	1,00E-22	3328855	22	6,80E-01	2688288	152	8,00E-39
YcaJ	g1787119	1460081	329	3,00E-91	3328753	60	1,00E-10	2688379	55	4,00E-09
b1808	g1788110	1340095	274	1,00E-74	3329029	27	9,30E-01	2688551	30	1,30E-01
yeaA	g1786464	1550715	126	8,00E-31	3328854	27	2,20E-01	2688358	23	3,80E+00
yqjF	g1788294	2213526	195	1,00E-50	3329033	28	7,30E-01	2688576	25	4,40E+00
b1983		2281051	124	8,00E-30	3328890	118	1,00E-28	2687898	138	1,00E-34
YnfD	g1406661	2808707	73	1,00E-13	3328908	56	2,00E-08	2688025	52	3,00E-07

Fig. 3 continued

E. coli gene name	GenBank#[1]	T. pallidum GenBank#[1]	score	E-value	S. pneumoniae[a] contig#[4]	score	E-value	S. aureus[a] contig#[4]	score	E-value
YgbB	gi1789103	3322804	98	1,00E-22	/	n.d.	n.d.	/	n.d.	n.d.
YihC	gi1788911	3322548	33	4,00E-03	101	71	2,00E-12	49	102	2,00E-25
YacE	gi1786292	3322572	36	6,00E-04	17	109	3,00E-24	/	n.d.	n.d.
YchB	gi1787459	3322649	83	7,00E-18	/	n.d.	n.d.	/	n.d.	n.d.
YejD	gi1788510	3322747	97	3,00E-22	41	166	2,00E-41	12	152	5,00E-37
Ydl	gi1789804	/	n.d.	n.d.	7	80	2,00E-15	249	82	9,00E-16
YggJ	gi1789315	3322550	27	4,90E-01	93	65	1,00E-10	90	86	7,00E-17
YjeE	gi1790610	3323187	76	6,00E-16	140	80	2,00E-15	24	75	9,00E-14
YfaO	gi1790004	3322488	28	2,00E-01	/	n.d.	n.d.	/	n.d.	n.d.
YhtC	gi2367210	3322447	39	6,00E-05	123	62	9,00E-10	193	76	3,00E-14
YihC	gi1789561	3322709	26	4,40E-01	47	55	8,00E-08	173	90	1,00E-18
YgbP	gi1789104	3322804	58	2,00E-10	72	55	2,00E-07	/	n.d.	n.d.
YbeY	gi1786880	3322948	48	1,00E-07	17	60	2,00E-09	396	75	7,00E-14
GcpE	gi1788863	3322731	217	3,00E-58	/	n.d.	n.d.	/	n.d.	n.d.
KdtB	gi1790065	3322553	100	2,00E-23	232	113	2,00E-25	205	149	2,00E-36
pfs	gi1786354	3322437	112	9,00E-27	156	182	5,00E-46	1235	82	1,00E-15
YcaJ	gi1787119	3323329	53	1,00E-08	62	95	2,00E-23	1085	159	1,00E-38
b1808	gi1788110	3322379	29	3,50E-01	114	114	5,00E-25	434	34	7,40E-01
yeaA	gi1788077	3322932	111	1,00E-26	31	136	2,00E-33	422	112	1,00E-25
yagF	gi1786464	3322975	26	3,20E+00	38	202	1,00E-51	24	171	4,00E-42
b1983	gi1788294	3322762	142	9,00E-36	143	360	1,00E-99	412	183	2,00E-46
YitD	gi1140861	Treponema	71	4,00E-13	12	64	7,00E-11	1341	76	1,00E-14

Fig. 3 continued

E. coli		E. faecalis*			P. aeruginosa*			B. pertussis*		
gene name	GenBank#[1]	contig#[4]	score	E-value	contig#[4]	score	E-value	contig#[4]	score	E-value
YqhB	g1789103	6177	141	8,00E-34	93	181	5,00E-46	126	139	3,00E-33
YhiC	g1788911	6349	132	3,00E-31	93	151	7,00E-37	737	151	9,00E-37
YacE	g1786292	6196	111	1,00E-24	95	187	1,00E-47	924	159	3,00E-39
YchB	g1787459	6342	114	2,00E-25	95	286	2,00E-77	1062	215	9,00E-56
YqjD	g1788510	6178	137	2,00E-32	94	198	8,00E-51	983	91	1,00E-18
Yrfl	g1789804	6199	97	2,00E-20	97	192	4,00E-49	1085	160	2,00E-39
YqjJ	g1789315	6287	75	1,00E-13	66	196	4,00E-50	551	119	4,00E-27
Yjel	g1790610	6294	29	4,60E+00	97	177	7,00E-45	762	125	4,00E-29
YiaO	g1790004	6236	125	1,00E-28	91	139	8,00E-33	459	201	1,00E-51
YidC	g2367210	6288	96	4,00E-20	75	163	2,00E-40	362	43	4,00E-05
YhbC	g1789561	6465	103	2,00E-22	85	148	6,00E-36	371	76	4,00E-14
YqjP	g1789104	6311	55	2,00E-07	93	180	2,00E-45	126	93	5,00E-19
YbuY	g1786800	6286	67	1,00E-11	91	142	3,00E-34	369	89	5,00E-18
GcpE	g1788863	/	n.d.	n.d.	91	514	1,00E-145	862	161	2,00E-39
KdtB	g1790065	6384	147	1,00E-35	84	197	1,00E-50	1097	172	2,00E-43
pls	g1786354	6495	201	1,00E-51	/	n.d.	n.d.	/	n.d.	n.d.
YcaJ	g1787119	6287	138	2,00E-32	89	529	1,00E-150	1043	452	1,00E-127
b1808	g1788110	6265	120	7,00E-27	82	215	1,00E-55	781	255	1,00E-67
yeaA	g1788077	6315	138	3,00E-33	81	158	2,00E-39	777	146	1,00E-35
yagF	g1788464	/	n.d.	n.d.	84	169	1,00E-41	759	160	8,00E-39
b1983	g1788294	6169	309	3,00E-84	82	145	5,00E-35	1059	155	6,00E-38
Yidl	g140861	/	n.d.	n.d.	46	76	1,00E-14	1007	74	7,00E-14

Fig. 3 continued

E. coli

gene name	GenBank#	B. subtilis GenBank#[1]	score	E-value	H. influenzae GenBank#[1]	score	E-value	H. pylori GenBank#[1]	score	E-value
yceG	g1787339	g2635201	140	2e-32	g1073838	289	2e-77	gbAAD07652.1	87	3e-16
yjbC	g396357	g2634751	132	3e-30	g1574128	101	7e-21	g2314637	99	4e-20

E. coli

gene name	GenBank#	M. tuberculosis GenBank#[1]	score	E-value	Ch. trachomatis GenBank#[1]	score	E-value	B. burgdorferi GenBank#[1]	score	E-value
yceG	g1787339	embCAB06185	74	2e-12	/	n.d.	n.d.	g2688649	101	1e-20
yjbC	g396357	g2326754	110	1e-23	g3329180	132	2e-30	g2688006	91	1e-17

E. coli

gene name	GenBank#	T. pallidum GenBank#[1]	score	E-value	S. pneumoniae contig#[4]	score	E-value	S. aureus contig#[4]	score	E-value
yceG	g1787339	g3322780	108	7e-23	/	n.d.	n.d.	/	n.d.	n.d.
yjbC	g396357	g3322747	90	2e-17	12	141	5e-34	4402	134	5e-32

E. coli

gene name	GenBank#	E. faecalis contig#[4]	score	E-value	P. aeruginosa contig#[4]	score	E-value	B. pertussis contig#[4]	score	E-value
yceG	g1787339	6216	115	4e-26	54	231	7e-61	398	209	2e-54
yjbC	g396357	6178	118	4e-27	54	109	2e-24	190	123	9e-29

Fig: 3 continued

Multiple sequence alignment of E. coli gene ygbB with 5 orthologs from different organisms

Legend: 1 = Escherichia coli; 2 = Haemophilus influenzae;
3 = Bacillus subtilis; 4 = Synechocystis; 5 = Treponema pallidum;
6 = Helicobacter pylori; 7 = Alignment score (* identical :
chemically similar . sterically similar)

```
1  --------------------------------------------------------------
2  --------------------------------------------------------------
3  --------------------------------------------------------------
4  --------------------------------------------------------------
5  MRRGGACVQKKEYLPLTSRQPGVCLLSEILVRALEARSFFLVVTVPAGEVAYAESQVAC
6  -MSLIRVNGEAFKLSLESLEEDPFETKETLETLIKQTSVVLLAAGESRRFSQTIKKQWLR
7  --------------------------------------------------------------
```

```
1  --------------------------------------------------------------
2  --------------------------------------------------------------
3  --------------------------------------------------------------
4  --------------------------------------------------------------
5  DSRLSAFPSRTRPVILYVPGAHTRSASVRAGLDAMATHAPDVVLVHDGARPFVSVALIHS
6  SNHTPLWLSVYESFKEALDFKEIILVVSELDYIYIKRHYPEIKLVKGGASRQESVRNALK
7  --------------------------------------------------------------
```

Fig. 4

```
1    ------------------------------------------------------------
2    ------------------------------------------------------------
3    ------------------------------------------------------------
4    ------------------------------------------------------------
5    VLEATCRYGAAVPVIEATDTPKGVAADGSIETHLIRSRVRLAQTPQGFCYASLCAAHHRA
6    IIDSAYTLTSDVARGLANIEALKNLFLTLQQTSHYCIAPYLPCYDTAIYYNEALDREAIK
7    ------------------------------------------------------------


1    ------------------------------------------------------------
2    ------------------------------------------------------------
3    ------------------------------------------------------------
4    ------------------------------------------------------------
5    ATDGEQYTDDSELYARYG-----GTVHVCAGERSNVKITYPEDLEQRASEPALTRGISVL
6    LIQTPQLSHTKALQSALNQGDFKDESSAILQAFPDRVSYIEGSKDLHKLTTSGDLKHFTL
7    ------------------------------------------------------------


1    ------MRIGHGFDVHAFGGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAA
2    ------MIRIGHGFDVHAFGEDRPLIIGGVEVPYHTGFIAHSDGDVALHALTDAILGAAA
3    ------MFRIGQGFDVHQLVEGRPLIIGGIEIPYEKGLLGHSDADVLLHTVADACLGAVG
4    ------MTALRIGNGYDIHRLVGDRPLILGGVTIAHHLGLDGHSDADVLTHALMDALLGALS
5    PCTEEGALRVGLGTDMHALCAGRPLILAGIHIPSKKGAQGHSDADVLAHASIDALLGAAG
6    FFNPAKDTFIGMGFDTHAFIKDKPMVLGGVVLDCEFGLKAHSDGDALLHAVIDAILGAIK
7         :  *   * *   * *    ..   :   :::.*:   .    .      *  .  ***.*.    **   **  ***
```

```
1 LGDIGKLFPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMR
2 LGDIGKLFPDTDMQYKNADSRGLLREAFRQVEKGYKIGNVDITIIAQAPKMRPHIDAMR
3 EGDIGKHFPDTDPEFKDADSFKLLQHVWGIVKQKGYVLGNIDCTIIAQKPKMLPYIEDMR
4 LGDIGHYFPPSDARWQGADSLKLLAQVHQLILERGWRINNLDNVIVAEQPKLKPHIQAMK
5 LGDIGTFFPSCDGRWKDAHSCALLRHTWQLVRAACWRLVNLDAVVCLEQPALHPFREAMR
6 GGDIGEWFPDNDPKYKNASSKELLKIVLDFSQSIGFELFEMGATIFSEIPKITPYKPAIL
7
  ****  *   *     ::. *       ..  ..  ::.  .. *   :. .

1 VFIAEDLGCHMDDVNVKATTEKLGFTGRGEGIACEAVALLIKATK-
2 AKIAEDLQCDIEQVNVKATTEKLGFTGRQEGIACEAVALLIRQ---
3 KRIAEGLEADVSQVNVKATTEKLGFTGRAEGIAAQATVLIQKG---
4 ENLAKVLTIDPDLIGKATTNERLGPTGREEGIAAYSVALLIKEG--
5 ASLAQALDTHVTRVFVKAKTAERLGPVGSGAAVTAQVVVLLKKI---
6 ENLSQLLGLEKSQISLKATTMEKMGFIGKQEGLLVQAHVSMRYKQKL
7 (
  :  ::     .    .  :**.  * *  :.: *          ..    .
```